

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/600,187A
Source: IFW16
Date Processed by STIC: 09/06/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/06/2006

PATENT APPLICATION: US/10/600,187A

TIME: 15:37:05

Input Set : N:\Crif3\RU0060\10500187A.RAW.txt

Output Set: N:\CRF4\09062006\J600187A.raw

1 <110> APPLICANT: O'Brien, Timothy J.
 2 <120> TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
 3 Overexpressed in Carcinomas
 4 <130> FILE REFERENCE: D6064CIP
 5 <140> CURRENT APPLICATION NUMBER: US/10/600,187A
 6 <141> CURRENT FILING DATE: 2003-06-20
 7 <150> PRIOR APPLICATION NUMBER: US/09/421,213
 8 <151> PRIOR FILING DATE: 1998-10-20
 9 <150> PRIOR APPLICATION NUMBER: US 09/027,337
 W--> 10 <151> PRIOR FILING DATE: 02-20-1998
 11 <160> NUMBER OF SEQ ID NOS: 98
 12 <170> SOFTWARE: MS Word 98
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 3147
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
 18 <220> FEATURE:
 19 <223> OTHER INFORMATION: TADG-15
 20 <400> SEQUENCE: 1
 21 tcaagagcgg cctcggggta ccatggggag cgatcggggc cgcaagggcg gagggggccc 60
 22 gaaggacttc ggcgcgggac tcaagtacaa ctcccggcac gagaaagtga atggcttgga 120
 23 ggaaggcgtg gagttcctgc cagtcaacaa cgtcaagaag gtggaaaagc atggcccggg 180
 24 gcgctgggtg gtgctggcag ccgtgctgat cggcctcctc ttggtcttgc tggggatcgg 240
 25 ctctcctggtg tggcatttgc agtaccggga cgtgcgtgtc cagaaggtct tcaatggcta 300
 26 catgaggatc acaaatgaga attttgtgga tgcctacgag aactccaact ccactgagtt 360
 27 tgtaagcctg gccagcaagg tgaaggacgc gctgaagctg ctgtacagcg gagtccatt 420
 28 cctgggcccc taccacaagg agtcggctgt gacggccttc agcgagggca gcgtcatcgc 480
 29 ctactactgg tctgagttca gcatcccgca gcacctggtg gaggaggccg agcgcgtcat 540
 30 ggccgaggag cgcgtagtca tgctgcccc gcgggcgcgc tccctgaagt cctttgtggt 600
 31 cacctcagtg gtggctttcc ccacggactc caaaacagta cagaggaccc aggacaacag 660
 32 ctgcagcttt ggctgcacg cccgcggtgt ggagctgatg cgcttcacca cggccggctt 720
 33 ccctgacagc ccctaccccg ctcatgccc ctgccagtgg gccctgcggg gggacgccga 780
 34 ctcagtgtctg agcctcacct tccgcagctt tgaccttgcg tccctgcgacg agcgcggcag 840
 35 cgacctgggtg acggtgtaca acaccctgag ccccatggag cccacgccc tgggtgcagtt 900
 36 gtgtggcacc taccctccct cctacaacct gacctccac tccctcccaga acgtcctgct 960
 37 catcacactg ataaccaaca ctgagcggcg gcatcccggc tttgaggcca ccttcttcca 1020
 38 gctgcctagg atgagcagct gtggaggccg cttacgtaaa gcccagggga cattcaacag 1080
 39 ccctactac ccaggccact acccacccaa cattgactgc acatggaaca ttgaggtgcc 1140
 40 caacaaccag catgtgaagg tgagcttcaa attcttctac ctgctggagc ccggcgtgcc 1200
 41 tgcgggcacc tgccccaagg actacgtgga gatcaatggg gagaaatact gcggagagag 1260
 42 gtccagttc gtcgtcacca gcaacagcaa caagatcaca gttcgcttcc actcagatca 1320
 43 gtccctacac gacaccggct tcttagctga atacctctcc tacgactcca gtgacccatg 1380
 44 cccggggcag ttcacgtgcc gcacggggcg gtgtatccgg aaggagctgc gctgtgatgg 1440

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45      ctgggccgac tgcaccgacc acagcgatga gctcaactgc agttgcgacg cgggccacca 1500
46      gttcacgtgc aagaacaagt tctgcaagcc cctcttctgg gtctgcgaca gtgtgaacga 1560
47      ctgcggagac aacagcgacg agcaggggtg cagttgtccg gcccagacct tcaggtgttc 1620
48      caatgggaag tgctctcga aaagccagca gtgcaatggg aaggacgact gtggggacgg 1680
49      gtccgacgag gcctcctgcc ccaaggtgaa cgtcgtcact tgtaccaaac acacctaccg 1740
50      ctgcctcaat gggctctgct tgagcaaggg caaccctgag tgtgacggga aggaggactg 1800
51      tagcgacggr tcagatgaga aggactgcga ctgtgggctg cggtcattca cgagacaggc 1860
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53      tgctctgggc cagggccaca tctgcggtgc ttccctcatc tctcccaact ggctgggtctc 1980
54      tgccgcacac tgctacatcg atgacagagg attcaggtac tcagacccca cgcagtggac 2040
55      ggcttctctg ggcttgacg accagagcca gcgcagcgcc cctggggtgc aggagcgcag 2100
56      gctcaagcgc atcatctccc acccttctt caatgacttc accttcgact atgacatcgc 2160
57      gctgctggag ctggagaaaac cggcagagta cagctccatg gtgcggccca tctgcctgcc 2220
58      ggagcctcc catgtcttcc ctgccggcaa ggccatctgg gtcacgggct ggggacacac 2280
59      ccagtatgga ggcactggcg cgctgatcct gcaaaaagggt gagatccgcg tcatcaacca 2340
60      gaccacctgc gagaacctcc tgccgcagca gatcacgccc cgcatgatgt gcgtgggctt 2400
61      cctcagcggc ggcgtggact cctgccaggg tgattccggg ggacccctgt ccagcgtgga 2460
62      ggcggatggg cggatcttcc aggccgtgt ggtgagctgg ggagacggct gcgctcagag 2520
63      gaacaagcca ggcgtgtaca caggctccc tctgtttcgg gactggatca aagagaacac 2580
64      tggggtatag gggccggggc caccctaatg tgtacacctg cggggccacc catcgtccac 2640
65      cccagtgtgc acgcctgcag gctggagact ggaccgctga ctgcaccagc gccccagaa 2700
66      catacactgt gaactcaatc tccagggtc caaatctgcc tagaaaacct ctgccttctc 2760
67      cagcctccaa agtggagctg ggaggtagaa ggggaggaca ctggtggttc tactgacca 2820
68      actgggggca aaggtttgaa gacacagcct ccccgccag ccccaagctg ggccgaggcg 2880
69      cgtttgtgta tatctgcctc cctgtctgt aaggagcagc gggaacggag cttcggagcc 2940
70      tcctcagtga aggtggtggg gctgccggat ctgggctgtg gggcccttgg gccacgctct 3000
71      tgaggaagcc caggctcgga ggacctgga aaacagacgg gtctgagact gaaattgttt 3060
72      taccagctcc cagggtggac ttcagtgtgt gtatttgtgt aaatgggtaa aacaatttat 3120
73      ttcttttttaa aaaaaaaaaa aaaaaaa 3147

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75 <210> SEQ ID NO: 2

76 <211> LENGTH: 855

77 <212> TYPE: PRT

78 <213> ORGANISM: Homo sapiens

79 <220> FEATURE:

80 <223> OTHER INFORMATION: TADG-15

81 <400> SEQUENCE: 2

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82      Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp
83              5              10              15
84      Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn
85              20              25              30
86      Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys
87              35              40              45
88      Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala
89              50              55              60
90      Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu
91              65              70              75
92      Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe
93              80              85              90
94      Asn Gly Tyr Met Arg Ile Thr Asn Glu Asn Phe Val Asp Ala Tyr

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Input Set : N:\Crif3\RULE60\10600187A.RAW.txt

Output Set: N:\CRF4\09062006\J600187A.raw

95		95		100		105
96	Glu Asn Ser Asn Ser Thr Glu Phe Val Ser Leu Ala Ser Lys Val					
97		110		115		120
98	Lys Asp Ala Leu Lys Leu Leu Tyr Ser Gly Val Pro Phe Leu Gly					
99		125		130		135
100	Pro Tyr His Lys Glu Ser Ala Val Thr Ala Phe Ser Glu Gly Ser					
101		140		145		150
102	Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser Ile Pro Gln His Leu					
103		155		160		165
104	Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu Arg Val Val Met					
105		170		175		180
106	Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val Val Thr Ser					
107		185		190		195
108	Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg Thr Gln					
109		200		205		210
110	Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu Leu					
111		215		220		225
112	Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala					
113		230		235		240
114	His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val					
115		245		250		255
116	Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu					
117		260		265		270
118	Arg Gly Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met					
119		275		280		285
120	Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser					
121		290		295		300
122	Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr					
123		305		310		315
124	Leu Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr					
125		320		325		330
126	Phe Phe Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg					
127		335		340		345
128	Lys Ala Gln Gly Thr Phe Asn Ser Pro Tyr Tyr Pro Gly His Tyr					
129		350		355		360
130	Pro Pro Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn					
131		365		370		375
132	Gln His Val Lys Val Ser Phe Lys Phe Phe Tyr Leu Leu Glu Pro					
133		380		385		390
134	Gly Val Pro Ala Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn					
135		395		400		405
136	Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe Val Val Thr Ser					
137		410		415		420
138	Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp Gln Ser Tyr					
139		425		430		435
140	Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp Ser Ser					
141		440		445		450
142	Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys Ile					
143		455		460		465

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Output Set: N:\CRF4\09062006\J600187A.raw

144	Arg	Lys	Glu	Leu	Arg	Cys	Asp	Gly	Trp	Ala	Asp	Cys	Thr	Asp	His
145					470					475					480
146	Ser	Asp	Glu	Leu	Asn	Cys	Ser	Cys	Asp	Ala	Gly	His	Gln	Phe	Thr
147					485					490					495
148	Cys	Lys	Asn	Lys	Phe	Cys	Lys	Pro	Leu	Phe	Trp	Val	Cys	Asp	Ser
149					500					505					510
150	Val	Asn	Asp	Cys	Gly	Asp	Asn	Ser	Asp	Glu	Gln	Gly	Cys	Ser	Cys
151					515					520					525
152	Pro	Ala	Gln	Thr	Phe	Arg	Cys	Ser	Asn	Gly	Lys	Cys	Leu	Ser	Lys
153					530					535					540
154	Ser	Gln	Gln	Cys	Asn	Gly	Lys	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp
155					545					550					555
156	Glu	Ala	Ser	Cys	Pro	Lys	Val	Asn	Val	Val	Thr	Cys	Thr	Lys	His
157					560					565					570
158	Thr	Tyr	Arg	Cys	Leu	Asn	Gly	Leu	Cys	Leu	Ser	Lys	Gly	Asn	Pro
159					575					580					585
160	Glu	Cys	Asp	Gly	Lys	Glu	Asp	Cys	Ser	Asp	Gly	Ser	Asp	Glu	Lys
161					590					595					600
162	Asp	Cys	Asp	Cys	Gly	Leu	Arg	Ser	Phe	Thr	Arg	Gln	Ala	Arg	Val
163					605					610					615
164	Val	Gly	Gly	Thr	Asp	Ala	Asp	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Val
165					620					625					630
166	Ser	Leu	His	Ala	Leu	Gly	Gln	Gly	His	Ile	Cys	Gly	Ala	Ser	Leu
167					635					640					645
168	Ile	Ser	Pro	Asn	Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Tyr	Ile	Asp
169					650					655					660
170	Asp	Arg	Gly	Phe	Arg	Tyr	Ser	Asp	Pro	Thr	Gln	Trp	Thr	Ala	Phe
171					665					670					675
172	Leu	Gly	Leu	His	Asp	Gln	Ser	Gln	Arg	Ser	Ala	Pro	Gly	Val	Gln
173					680					685					690
174	Glu	Arg	Arg	Leu	Lys	Arg	Ile	Ile	Ser	His	Pro	Phe	Phe	Asn	Asp
175					695					700					705
176	Phe	Thr	Phe	Asp	Tyr	Asp	Ile	Ala	Leu	Leu	Glu	Leu	Glu	Lys	Pro
177					710					715					720
178	Ala	Glu	Tyr	Ser	Ser	Met	Val	Arg	Pro	Ile	Cys	Leu	Pro	Asp	Ala
179					725					730					735
180	Ser	His	Val	Phe	Pro	Ala	Gly	Lys	Ala	Ile	Trp	Val	Thr	Gly	Trp
181					740					745					750
182	Gly	His	Thr	Gln	Tyr	Gly	Gly	Thr	Gly	Ala	Leu	Ile	Leu	Gln	Lys
183					755					760					765
184	Gly	Glu	Ile	Arg	Val	Ile	Asn	Gln	Thr	Thr	Cys	Glu	Asn	Leu	Leu
185					770					775					780
186	Pro	Gln	Gln	Ile	Thr	Pro	Arg	Met	Met	Cys	Val	Gly	Phe	Leu	Ser
187					785					790					795
188	Gly	Gly	Val	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ser
189					800					805					810
190	Ser	Val	Glu	Ala	Asp	Gly	Arg	Ile	Phe	Gln	Ala	Gly	Val	Val	Ser
191					815					820					825
192	Trp	Gly	Asp	Gly	Cys	Ala	Gln	Arg	Asn	Lys	Pro	Gly	Val	Tyr	Thr

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193          830          835          840
194      Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val
195          845          850          855
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 256
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Hepsin
203 <400> SEQUENCE: 3
204      Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro Trp
205          5          10          15
206      Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser
207          20          25          30
208      Leu Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro
209          35          40          45
210      Glu Arg Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala
211          50          55          60
212      Val Ala Gln Ala Ser Pro His Gly Leu Gln Leu Gly Val Cln Ala
213          65          70          75
214      Val Val Tyr His Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser
215          80          85          90
216      Glu Glu Asn Ser Asn Asp Ile Ala Leu Val His Leu Ser Ser Pro
217          95          100          105
218      Leu Pro Leu Thr Glu Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala
219          110          115          120
220      Gly Gln Ala Leu Val Asp Gly Lys Ile Cys Thr Val Thr Gly Trp
221          125          130          135
222      Gly Asn Thr Gln Tyr Tyr Gly Gln Gln Ala Gly Val Leu Gln Glu
223          140          145          150
224      Ala Arg Val Pro Ile Ile Ser Asn Asp Val Cys Asn Gly Ala Asp
225          155          160          165
226      Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met Phe Cys Ala Gly Tyr
227          170          175          180
228      Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro
229          185          190          195
230      Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg Trp Arg Leu
231          200          205          210
232      Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala Gln Lys
233          215          220          225
234      Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp Ile Phe
235          230          235          240
236      Gln Ala Ile Lys Thr His Ser Glu Ala Ser Gly Met Val Thr Gln
237          245          250          255
238      Leu
240 <210> SEQ ID NO: 4
241 <211> LENGTH: 225
242 <212> TYPE: PRT
243 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/06/2006
PATENT APPLICATION: US/10/600,187A TIME: 15:37:06

Input Set : N:\Crf3\RULE60\10600187A.RAW.txt
Output Set: N:\CRF4\09062006\J600187A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 6,9,12,15,18

Seq#:12; N Pos. 3,6,9,12,18

VERIFICATION SUMMARY

DATE: 09/06/2006

PATENT APPLICATION: US/10/600,187A

TIME: 15:37:06

Input Set : N:\Crf3\RULE60\10600187A.RAW.txt

Output Set: N:\CRF4\09062006\J600187A.raw

L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:631 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:642 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0